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## SEQUENCE LISTING

&lt;110&gt; TORAY INDUSTRIES, INC.

<120> Agent for therapy and/or prevention of kidney diseases and method  
for diagnosing kidney diseases

&lt;130&gt; 02796

&lt;160&gt; 27

&lt;210&gt; 1

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> antisense oligonucleotide used for inhibition of casein kinase 2  
 $\alpha$  subunit gene

&lt;400&gt; 1

gtaatcatct tgattacccc a 21

&lt;210&gt; 2

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> antisense oligonucleotide used for inhibition of casein kinase 2  
 $\beta$  subunit gene

&lt;400&gt; 2

ggttggcgg ccgcttgggc c 21

&lt;210&gt; 3

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&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> antisense oligonucleotide used for inhibition of casein kinase 2  
 $\alpha'$  subunit gene

&lt;400&gt; 3

ttcaaatacc aaagctggtg

20

&lt;210&gt; 4

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> antisense oligonucleotide used for inhibition of casein kinase 2  
 $\alpha'$  subunit gene

&lt;400&gt; 4

atcaaagtct gtcaggatct

20

&lt;210&gt; 5

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> antisense oligonucleotide used for inhibition of casein kinase 2  
 $\alpha'$  subunit gene

&lt;400&gt; 5

tggataaagt tttcccagcg

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<210> 6

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense oligonucleotide used for inhibition of casein kinase 2  
 $\alpha'$  subunit gene

<400> 6

accaagtttt cgaacccagt t

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<210> 7

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense oligonucleotide used for inhibition of casein kinase 2  
 $\beta$  subunit gene

<400> 7

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<210> 8

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense oligonucleotide used for inhibition of casein kinase 2  
 $\beta$  subunit gene

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&lt;400&gt; 8

ctcagagcta aagcctcgtg

20

&lt;210&gt; 9

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; antisense oligonucleotide used for inhibition of casein kinase 2

 $\beta$  subunit gene

&lt;400&gt; 9

acccgaccgc ggcaggcgaa

20

&lt;210&gt; 10

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; antisense oligonucleotide used for inhibition of casein kinase 2

 $\beta$  subunit gene

&lt;400&gt; 10

gcggcgaccg ctacagcgca

20

&lt;210&gt; 11

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

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<223> oligonucleotide primer used for PCR for amplification of rat case  
in kinase 2  $\beta$  subunit gene

<400> 11

ccgcggacat aaagatgagt

20

<210> 12

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer used for PCR for amplification of rat case  
in kinase 2  $\beta$  subunit gene

<400> 12

aaaccagtgc cgaagtatgc

20

<210> 13

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer used for PCR for amplification of rat case  
in kinase 2  $\alpha$  subunit gene

<400> 13

agaaagcttc ggctaataga

20

<210> 14

<211> 20

<212> DNA

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&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> oligonucleotide primer used for PCR for amplification of rat case  
in kinase 2  $\alpha$  subunit gene

&lt;400&gt; 14

actgaagaaa tccctgacat 20

&lt;210&gt; 15

&lt;211&gt; 2187

&lt;212&gt; DNA

&lt;213&gt; homo sapiens

&lt;400&gt; 15

gagcagaggg gagacggcgg ccgccctggc cgcttccacc acagtttgaa gaaaacaggt 60

ctgaaacaag gtcttacccc cagctgcttc tgaacacagt gactgccaga tctccaaaca 120

tcaagtccag ctttgtccgc caacctgtct gac atg tcg gga ccc gtg cca agc 174

Met Ser Gly Pro Val Pro Ser

1

5

agg gcc aga gtt tac aca gat gtt aat aca cac aga cct cga gaa tac 222

Arg Ala Arg Val Tyr Thr Asp Val Asn Thr His Arg Pro Arg Glu Tyr

10

15

20

tgg gat tac gag tca cat gtg gtg gaa tgg gga aat caa gat gac tac 270

Trp Asp Tyr Glu Ser His Val Val Glu Trp Gly Asn Gln Asp Asp Tyr

25

30

35

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cag ctg gtt cga aaa tta ggc cga ggt aaa tac agt gaa gta ttt gaa 318  
Gln Leu Val Arg Lys Leu Gly Arg Gly Lys Tyr Ser Glu Val Phe Glu  
40 45 50 55

gcc atc aac atc aca aat aat gaa aaa gtt gtt gtt aaa att ctc aag 366  
Ala Ile Asn Ile Thr Asn Asn Glu Lys Val Val Val Lys Ile Leu Lys  
60 65 70

cca gta aaa aag aag aaa att aag cgt gaa ata aag att ttg gag aat 414  
Pro Val Lys Lys Lys Lys Ile Lys Arg Glu Ile Lys Ile Leu Glu Asn  
75 80 85

ttg aga gga ggt ccc aac atc atc aca ctg gca gac att gta aaa gac 462  
Leu Arg Gly Gly Pro Asn Ile Ile Thr Leu Ala Asp Ile Val Lys Asp  
90 95 100

cct gtg tca cga acc ccc gcc ttg gtt ttt gaa cac gta aac aac aca 510  
Pro Val Ser Arg Thr Pro Ala Leu Val Phe Glu His Val Asn Asn Thr  
105 110 115

gac ttc aag caa ttg tac cag acg tta aca gac tat gat att cga ttt 558  
Asp Phe Lys Gln Leu Tyr Gln Thr Leu Thr Asp Tyr Asp Ile Arg Phe  
120 125 130 135

tac atg tat gag att ctg aag gcc ctg gat tat tgt cac agc atg gga 606  
Tyr Met Tyr Glu Ile Leu Lys Ala Leu Asp Tyr Cys His Ser Met Gly  
140 145 150

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att atg cac aga gat gtc aag ccc cat aat gtc atg att gat cat gag 654

Ile Met His Arg Asp Val Lys Pro His Asn Val Met Ile Asp His Glu

155

160

165

cac aga aag cta cga cta ata gac tgg ggt ttg gct gag ttt tat cat 702

His Arg Lys Leu Arg Leu Ile Asp Trp Gly Leu Ala Glu Phe Tyr His

170

175

180

cct ggc caa gaa tat aat gtc cga gtt gct tcc cga tac ttc aaa ggt 750

Pro Gly Gln Glu Tyr Asn Val Arg Val Ala Ser Arg Tyr Phe Lys Gly

185

190

195

cct gag cta ctt gta gac tat cag atg tac gat tat agt ttg gat atg 798

Pro Glu Leu Leu Val Asp Tyr Gln Met Tyr Asp Tyr Ser Leu Asp Met

200

205

210

215

tgg agt ttg ggt tgt atg ctg gca agt atg atc ttt cgg aag gag cca 846

Trp Ser Leu Gly Cys Met Leu Ala Ser Met Ile Phe Arg Lys Glu Pro

220

225

230

ttt ttc cat gga cat gac aat tat gat cag ttg gtg agg ata gcc aag 894

Phe Phe His Gly His Asp Asn Tyr Asp Gln Leu Val Arg Ile Ala Lys

235

240

245

gtt ctg ggg aca gaa gat tta tat gac tat att gac aaa tac aac att 942

Val Leu Gly Thr Glu Asp Leu Tyr Asp Tyr Ile Asp Lys Tyr Asn Ile

250

255

260



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gaa tta gat cca cgt ttc aat gat atc ttg ggc aga cac tct cga aag 990

Glu Leu Asp Pro Arg Phe Asn Asp Ile Leu Gly Arg His Ser Arg Lys

265

270

275

cga tgg gaa cgc ttt gtc cac agt gaa aat cag cac ctt gtc agc cct 1038

Arg Trp Glu Arg Phe Val His Ser Glu Asn Gln His Leu Val Ser Pro

280

285

290

295

gag gcc ttg gat ttc ctg gac aaa ctg ctg cga tat gac cac cag tca 1086

Glu Ala Leu Asp Phe Leu Asp Lys Leu Leu Arg Tyr Asp His Gln Ser

300

305

310

cgg ctt act gca aga gag gca atg gag cac ccc tat ttc tac act gtt 1134

Arg Leu Thr Ala Arg Glu Ala Met Glu His Pro Tyr Phe Tyr Thr Val

315

320

325

gtg aag gac cag gct cga atg ggt tca tct agc atg cca ggg ggc agt 1182

Val Lys Asp Gln Ala Arg Met Gly Ser Ser Ser Met Pro Gly Gly Ser

330

335

340

acg ccc gtc agc agc gcc aat atg atg tca ggg att tct tca gtg cca 1230

Thr Pro Val Ser Ser Ala Asn Met Met Ser Gly Ile Ser Ser Val Pro

345

350

355

acc cct tca ccc ctt gga cct ctg gca ggc tca cca gtg att gct gct 1278

Thr Pro Ser Pro Leu Gly Pro Leu Ala Gly Ser Pro Val Ile Ala Ala

360

365

370

375

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gcc aac ccc ctt ggg atg cct gtt cca gct gcc gct ggc gct cag cag 1326

Ala Asn Pro Leu Gly Met Pro Val Pro Ala Ala Ala Gly Ala Gln Gln

380

385

390

taa cggccctatc tgtctcctga tgccctgagca gaggtggggg agtccaccct 1379

ctccttgatg cagcttgccg ctggcgggga ggggtgaaac acttcagaag caccgtgtct 1439

gaaccgttgc ttgtggattt atagtagttc agtcataaaa aaaaaaatta taataggctg 1499

atcttctttt ttcttttttt tttaactcga acttttcata actcagggga ttccctgaaa 1559

aattacctgc aggtggaata ttcatggac aatttttttt tctccctcc caaatttagt 1619

tcctcatcac aaaagaacaa agataaacca gccatcatcc cggctgctgc atttaggtgg 1679

agacttcttc ccattccac cattgttcct ccaccgtccc acactttagg gggttggtat 1739

ctcgtgctct tctccagaga ttacaaaaat gtagcttctc aggggaggca ggaagaaagg 1799

aaggaaggaa agaaggaagg gaggacccaa tctataggag cagtggactg cttgctggtc 1859

gcttacatca ctttactcca taagcgcttc agtggggtta tcttagtggc tcttgtggaa 1919

gtgtgtctta gttacatcaa gatgttaaaa tctacccaaa atgcagacag atactaaaac 1979

tctgtcagta gatcatgtct tactgatcta accctaaatc caactcattt atacttttat 2039

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ttttagttca gtttaaaatg ttgatacctt ccctcccagg ctccttacct tggctcttttc 2099

cctgttcacg tcccaacatg ctgtgctcca tagctggtag gagagggaag gcaaaatctt 2159

tcttagtttt ctttatctt 2178

<210> 16

<211> 1677

<212> DNA

<213> homo sapiens

<400> 16

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gttcaagcga ttctcctgcc tcttcgccc gacgcccgc gtcccccgc gcgcgcgcgc 120

cgcaccctc tgcgcccgc gccgcccc ggtcccgccc gcc atg ccc ggc cgc 175

Met Pro Gly Pro

1

gcc gcg ggc agc agg gcc cgg gtc tac gcc gag gtg aac agt ctg agg 223

Ala Ala Gly Ser Arg Ala Arg Val Tyr Ala Glu Val Asn Ser Leu Arg

5 10 15 20

agc cgc gag tac tgg gac tac gag gct cac gtc ccg agc tgg ggt aat 271

Ser Arg Glu Tyr Trp Asp Tyr Glu Ala His Val Pro Ser Trp Gly Asn

25 30 35

caa gat gat tac caa ctg gtt cga aaa ctt ggt cgg gga aaa tat agt 319

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Gln Asp Asp Tyr Gln Leu Val Arg Lys Leu Gly Arg Gly Lys Tyr Ser

40

45

50

gaa gta ttt gag gcc att aat atc acc aac aat gag aga gtg gtt gta 367

Glu Val Phe Glu Ala Ile Asn Ile Thr Asn Asn Glu Arg Val Val Val

55

60

65

aaa atc ctg aag cca gtg aag aaa aag aag ata aaa cga gag gtt aag 415

Lys Ile Leu Lys Pro Val Lys Lys Lys Lys Ile Lys Arg Glu Val Lys

70

75

80

att ctg gag aac ctt cgt ggt gga aca aat atc att aag ctg att gac 463

Ile Leu Glu Asn Leu Arg Gly Gly Thr Asn Ile Ile Lys Leu Ile Asp

85

90

95

100

act gta aag gac ccc gtg tca aag aca cca gct ttg gta ttt gaa tat 511

Thr Val Lys Asp Pro Val Ser Lys Thr Pro Ala Leu Val Phe Glu Tyr

105

110

115

atc aat aat aca gat ttt aag caa ctc tac cag atc ctg aca gac ttt 559

Ile Asn Asn Thr Asp Phe Lys Gln Leu Tyr Gln Ile Leu Thr Asp Phe

120

125

130

gat atc cgg ttt tat atg tat gaa cta ctt aaa gct ctg gat tac tgc 607

Asp Ile Arg Phe Tyr Met Tyr Glu Leu Leu Lys Ala Leu Asp Tyr Cys

135

140

145

cac agc aag gga atc atg cac agg gat gtg aaa cct cac aat gtc atg 655

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His Ser Lys Gly Ile Met His Arg Asp Val Lys Pro His Asn Val Met  
150 155 160

ata gat cac caa cag aaa aag ctg cga ctg ata gat tgg ggt ctg gca 703  
Ile Asp His Gln Gln Lys Lys Leu Arg Leu Ile Asp Trp Gly Leu Ala  
165 170 175 180

gaa ttc tat cat cct gct cag gag tac aat gtt cgt gta gcc tca agg 751  
Glu Phe Tyr His Pro Ala Gln Glu Tyr Asn Val Arg Val Ala Ser Arg  
185 190 195

tac ttc aag gga cca gag ctc ctc gtg gac tat cag atg tat gat tat 799  
Tyr Phe Lys Gly Pro Glu Leu Leu Val Asp Tyr Gln Met Tyr Asp Tyr  
200 205 210

agc ttg gac atg tgg agt ttg ggc tgt atg tta gca agc atg atc ttt 847  
Ser Leu Asp Met Trp Ser Leu Gly Cys Met Leu Ala Ser Met Ile Phe  
215 220 225

cga agg gaa cca ttc ttc cat gga cag gac aac tat gac cag ctt gtt 895  
Arg Arg Glu Pro Phe Phe His Gly Gln Asp Asn Tyr Asp Gln Leu Val  
230 235 240

cgc att gcc aag gtt ctg ggt aca gaa gaa ctg tat ggg tat ctg aag 943  
Arg Ile Ala Lys Val Leu Gly Thr Glu Glu Leu Tyr Gly Tyr Leu Lys  
245 250 255 260

aag tat cac ata gac cta gat cca cac ttc aac gat atc ctg gga caa 991

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Lys Tyr His Ile Asp Leu Asp Pro His Phe Asn Asp Ile Leu Gly Gln  
265 270 275

cat tca cgg aaa cgc tgg gaa aac ttt atc cat agt gag aac aga cac 1039  
His Ser Arg Lys Arg Trp Glu Asn Phe Ile His Ser Glu Asn Arg His  
280 285 290

ctt gtc agc cct gag gcc cta gat ctt ctg gac aaa ctt ctg cga tac 1087  
Leu Val Ser Pro Glu Ala Leu Asp Leu Leu Asp Lys Leu Leu Arg Tyr  
295 300 305

gac cat caa cag aga ctg act gcc aaa gag gcc atg gag cac cca tac 1135  
Asp His Gln Gln Arg Leu Thr Ala Lys Glu Ala Met Glu His Pro Tyr  
310 315 320

ttc tac cct gtg gtg aag gag cag tcc cag cct tgt gca gac aat gct 1183  
Phe Tyr Pro Val Val Lys Glu Gln Ser Gln Pro Cys Ala Asp Asn Ala  
325 330 335 340

gtg ctt tcc agt ggt ctc acg gca gca cga tga agactggaaa ggcaggggtc 1236  
Val Leu Ser Ser Gly Leu Thr Ala Ala Arg  
345 350

tgttgcggtt ctccacttt tccataagca gaacaagaac caaatcaaac gtcttaacgc 1296

gtatagagag atcacgttcc gtgagcagac acaaaacggt ggcaggtttg gcgagcacga 1356

actagaccaa ggaaggga gccaccacc gtatatcaaa cctcacttcc gaatgtaaaa 1416

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ggctcacttg cctttggctt cctgttgact tcttcccgac ccagaaagca tggggaatgt 1476

gaagggtatg cagaatgttg ttggttactg ttgctcccg agccctcaa ctogtcccg 1536

ggcgcctgt tttccagca aaccacgta actagctgac cacagactcc acagtggggg 1596

gacgggcgca gtatgtggca tggcggcagt tacatattat tattttaaaa gtatatatta 1656

ttgaataaaa ggttttaaaa g 1677

<210> 17

<211> 648

<212> DNA

<213> homo sapiens

<400> 17

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Met Ser Ser Ser Glu Glu Val Ser Trp Ile Ser Trp Phe Cys Gly Leu

1

5

10

15

cgt ggc aat gaa ttc ttc tgt gaa gtg gat gaa gac tac atc cag gac 96

Arg Gly Asn Glu Phe Phe Cys Glu Val Asp Glu Asp Tyr Ile Gln Asp

20

25

30

aaa ttt aat ctt act gga ctc aat gag cag gtc cct cac tat cga caa 144

Lys Phe Asn Leu Thr Gly Leu Asn Glu Gln Val Pro His Tyr Arg Gln

35

40

45

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gct cta gac atg atc ttg gac ctg gag cct gat gaa gaa ctg gaa gac 192  
Ala Leu Asp Met Ile Leu Asp Leu Glu Pro Asp Glu Glu Leu Glu Asp  
50 55 60

aac ccc aac cag agt gac ctg att gag cag gca gcc gag atg ctt tat 240  
Asn Pro Asn Gln Ser Asp Leu Ile Glu Gln Ala Ala Glu Met Leu Tyr  
65 70 75 80

gga ttg atc cac gcc cgc tac atc ctt acc aac cgt ggc atc gcc cag 288  
Gly Leu Ile His Ala Arg Tyr Ile Leu Thr Asn Arg Gly Ile Ala Gln  
85 90 95

atg ttg gaa aag tac cag caa gga gac ttt ggt tac tgt cct cgt gtg 336  
Met Leu Glu Lys Tyr Gln Gln Gly Asp Phe Gly Tyr Cys Pro Arg Val  
100 105 110

tac tgt gag aac cag cca atg ctt ccc att ggc ctt tca gac atc cca 384  
Tyr Cys Glu Asn Gln Pro Met Leu Pro Ile Gly Leu Ser Asp Ile Pro  
115 120 125

ggt gaa gcc atg gtg aag ctc tac tgc ccc aag tgc atg gat gtg tac 432  
Gly Glu Ala Met Val Lys Leu Tyr Cys Pro Lys Cys Met Asp Val Tyr  
130 135 140

aca ccc aag tca tca aga cac cat cac acg gat ggc gcc tac ttc ggc 480  
Thr Pro Lys Ser Ser Arg His His His Thr Asp Gly Ala Tyr Phe Gly  
145 150 155 160



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act ggt ttc cct cac atg ctc ttc atg gtg cat ccc gag tac cgg ccc 528  
 Thr Gly Phe Pro His Met Leu Phe Met Val His Pro Glu Tyr Arg Pro  
 165 170 175

aag aga cct gcc aac cag ttt gtg ccc agg ctc tac ggt ttc aag atc 576  
 Lys Arg Pro Ala Asn Gln Phe Val Pro Arg Leu Tyr Gly Phe Lys Ile  
 180 185 190

cat ccg atg gcc tac cag ctg cag ctc caa gcc gcc agc aac ttc aag 624  
 His Pro Met Ala Tyr Gln Leu Gln Leu Gln Ala Ala Ser Asn Phe Lys  
 195 200 205

agc cca gtc aag acg att cgc tga 648  
 Ser Pro Val Lys Thr Ile Arg  
 210 215

&lt;210&gt; 18

&lt;211&gt; 2180

&lt;212&gt; DNA

&lt;213&gt; rat

&lt;400&gt; 18

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 gtgggattcc tgctgtaagg gaagggatgt cataggtcag ttgaccaatg accagaccta 180  
 aacatggctc ccagccttag goatgcggag cctaggagtc ctttcaacco tggcctgtga 240  
 tttttccago tcagatgaca aagacatcta ggcccagtgt cttgagaatc cctatagtca 300  
 aggattagag tctctctcag tgagtcagct cccccagtca gtaccctcac aagatatcaa 360  
 ccgaattcgg tttttttttt tttttttttt taaatatgta aggcctttcaa tttattacag 420

18/26

atcacccaag aacataatga tatacatgta gtcagaaaaac acgatgtaga aatcatagtg	480
agttgtccag acatagtcag tagattattc tttctggcat gctccagtgt caagacctca	540
ataaagagca ctaaaatcct tccatacaat taagtatcag cgatgtacca tattgcagaa	600
aggggtggct gagcaacagt ttgttgatac tataagaatt ccatgctcaa cagtcgtagc	660
gttgcaactca gcacagctct ggtttccata tacaaatttt ccatctcgta ggggagcgcg	720
gctagtccg ctgccgttc caccgcagta actgccagat cttccaacat cacgttcagc	780
tttgtccgtc aacctgtctg ac atg tcg gga ccc gtg cca agc agg gcc aga	832
Met Ser Gly Pro Val Pro Ser Arg Ala Arg	
1 5 10	
gtt tac aca gat gtt aac aca cac aga ccc cga gag tac tgg gac tat	880
Val Tyr Thr Asp Val Asn Thr His Arg Pro Arg Glu Tyr Trp Asp Tyr	
15 20 25	
gaa tca cat gtg gtg gaa tgg gga aat caa gat gac tac cag ctt gtt	928
Glu Ser His Val Val Glu Trp Gly Asn Gln Asp Asp Tyr Gln Leu Val	
30 35 40	
cga aaa tta ggc agg ggc aaa tac agt gaa gtg ttt gag gcc atc aat	976
Arg Lys Leu Gly Arg Gly Lys Tyr Ser Glu Val Phe Glu Ala Ile Asn	
45 50 55	
atc aca aat aat gaa aaa gtt gtt gtt aaa att ctc aag cca gta aaa	1024
Ile Thr Asn Asn Glu Lys Val Val Val Lys Ile Leu Lys Pro Val Lys	
60 65 70	
aag aag aaa att aag cgt gaa ata aag att ttg gag aat tta aga ggt	1072
Lys Lys Lys Ile Lys Arg Glu Ile Lys Ile Leu Glu Asn Leu Arg Gly	
75 80 85 90	
ggg ccc aac atc atc aca ctt gca gac att gtg aaa gac cct gtg tot	1120
Gly Pro Asn Ile Ile Thr Leu Ala Asp Ile Val Lys Asp Pro Val Ser	
95 100 105	
cga acc cct gcc ttg gtt ttt gaa cat gta aac aac aca gac ttc aag	1168

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Arg Thr Pro Ala Leu Val Phe Glu His Val Asn Asn Thr Asp Phe Lys	
110 115 120	
caa ttg tac cag acg tta aca gac tat gac att cga ttt tac atg tat	1216
Gln Leu Tyr Gln Thr Leu Thr Asp Tyr Asp Ile Arg Phe Tyr Met Tyr	
125 130 135	
gaa att ctg aaa gcc ctg gat tat tgt cac agc atg ggg att atg cac	1264
Glu Ile Leu Lys Ala Leu Asp Tyr Cys His Ser Met Gly Ile Met His	
140 145 150	
aga gac gtg aaa ccg cat aat gtc atg att gat cat gag cac aga aag	1312
Arg Asp Val Lys Pro His Asn Val Met Ile Asp His Glu His Arg Lys	
155 160 165 170	
ctt cgg cta ata gat tgg ggt tta gca gag ttt tac cat cct ggc caa	1360
Leu Arg Leu Ile Asp Trp Gly Leu Ala Glu Phe Tyr His Pro Gly Gln	
175 180 185	
gag tat aat gtc cga gtt gct tcc cga tat ttc aaa ggt cca gag cta	1408
Glu Tyr Asn Val Arg Val Ala Ser Arg Tyr Phe Lys Gly Pro Glu Leu	
190 195 200	
ctt gta gat tat cag atg tac gat tat agt ttg gat atg tgg agc ttg	1456
Leu Val Asp Tyr Gln Met Tyr Asp Tyr Ser Leu Asp Met Trp Ser Leu	
205 210 215	
ggt tgt atg ctg gca agt atg atc ttc cgg aag gag cca ttt ttc cat	1504
Gly Cys Met Leu Ala Ser Met Ile Phe Arg Lys Glu Pro Phe Phe His	
220 225 230	
gga cat gac aat tat gat cag ttg gtg agg ata gcc aag gtt ctg gga	1552
Gly His Asp Asn Tyr Asp Gln Leu Val Arg Ile Ala Lys Val Leu Gly	
235 240 245 250	
acg gaa gat tta tat gac tat att gac aag tac aac att gaa tta gat	1600
Thr Glu Asp Leu Tyr Asp Tyr Ile Asp Lys Tyr Asn Ile Glu Leu Asp	

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255	260	265	
cca cgt ttc aac gat atc ttg ggc aga cac tcc cgt aag cga tgg gaa			1648
Pro Arg Phe Asn Asp Ile Leu Gly Arg His Ser Arg Lys Arg Trp Glu			
270	275	280	
cgc ttt gtc cac agt gaa aac cag cac ctt gtc agc ccc gag gcc ttg			1696
Arg Phe Val His Ser Glu Asn Gln His Leu Val Ser Pro Glu Ala Leu			
285	290	295	
gat ttt ctg gac aag ctg ctg cga tac gac cac cag tct cgg ctc act			1744
Asp Phe Leu Asp Lys Leu Leu Arg Tyr Asp His Gln Ser Arg Leu Thr			
300	305	310	
gca aga gag gcc atg gag cac cct tac ttc tac act gtc gtg aag gac			1792
Ala Arg Glu Ala Met Glu His Pro Tyr Phe Tyr Thr Val Val Lys Asp			
315	320	325	330
cag gct cga atg agt tcg gct ggc atg gca ggg ggc agc aca cct gtc			1840
Gln Ala Arg Met Ser Ser Ala Gly Met Ala Gly Gly Ser Thr Pro Val			
335	340	345	
agt agc gcc aat atg atg tca ggg att tct tca gtg cca acc cct tca			1888
Ser Ser Ala Asn Met Met Ser Gly Ile Ser Ser Val Pro Thr Pro Ser			
350	355	360	
ccc ctg gga cct ctg gca ggc tca ccc gtg att gct gct gcc aac tca			1936
Pro Leu Gly Pro Leu Ala Gly Ser Pro Val Ile Ala Ala Ala Asn Ser			
365	370	375	
ctt ggg ata ccc gta cca gct gcc gct ggc gct cag cag taa tgaccccat			1987
Leu Gly Ile Pro Val Pro Ala Ala Ala Gly Ala Gln Gln			
380	385	390	
ctgtcttctg atgcctgggc agaggtggga cgtccaccct ctccttaatg cagottgcgc			2047
ctggttggga ggggtgagaa cacttcagaa gcaccgtgtc tgaaccgttg cttgtggatt			2107
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tttaaaaaaa ccg

2180

&lt;210&gt; 19

&lt;211&gt; 1964

&lt;212&gt; DNA

&lt;213&gt; rat

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Met

1

agt agc tct gag gag gtg tcc tgg att tcc tgg ttc tgt ggg ctc cgt 164

Ser Ser Ser Glu Glu Val Ser Trp Ile Ser Trp Phe Cys Gly Leu Arg

5

10

15

ggc aat gaa ttc ttc tgt gag gtg gat gaa gac tac atc cag gac aaa 212

Gly Asn Glu Phe Phe Cys Glu Val Asp Glu Asp Tyr Ile Gln Asp Lys

20

25

30

ttt aat ctt act gga ctc aat gag cag gtg cct cac tat cga caa gcc 260

Phe Asn Leu Thr Gly Leu Asn Glu Gln Val Pro His Tyr Arg Gln Ala

35

40

45

cta gac atg atc ttg gac ctg gaa cct gat gaa gag ctg gaa gac aac 308

Leu Asp Met Ile Leu Asp Leu Glu Pro Asp Glu Glu Leu Glu Asp Asn

50

55

60

65

ccc aac cag agt gac ttg att gag cag gcg gcc gag atg ctc tat ggg 356

Pro Asn Gln Ser Asp Leu Ile Glu Gln Ala Ala Glu Met Leu Tyr Gly

70

75

80

ttg atc cac gcc cgc tac atc ctc acc aac cgg ggc att gca caa atg 404

Leu Ile His Ala Arg Tyr Ile Leu Thr Asn Arg Gly Ile Ala Gln Met

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85	90	95	
ttg gaa aag tac cag caa gga gac ttt ggc tac tgt cct cga gta tac			452
Leu Glu Lys Tyr Gln Gln Gly Asp Phe Gly Tyr Cys Pro Arg Val Tyr			
100	105	110	
tgt gag aac cag ccg atg ctt ccc atc ggc ctt tcg gac atc cca gga			500
Cys Glu Asn Gln Pro Met Leu Pro Ile Gly Leu Ser Asp Ile Pro Gly			
115	120	125	
gag gcc atg gtg aag ctc tac tgc ccc aag tgc atg gac gtg tac aca			548
Glu Ala Met Val Lys Leu Tyr Cys Pro Lys Cys Met Asp Val Tyr Thr			
130	135	140	145
ccc aag tcc tct agg cac cac cac acg gat ggc gca tac ttc ggc act			596
Pro Lys Ser Ser Arg His His His Thr Asp Gly Ala Tyr Phe Gly Thr			
150	155	160	
ggt ttc cct cac atg ctc ttc atg gtg cat ccc gag tac cgg ccc aag			644
Gly Phe Pro His Met Leu Phe Met Val His Pro Glu Tyr Arg Pro Lys			
165	170	175	
cgg ccg gcc aac cag ttt gtg ccc agg ctc tac ggt ttc aag atc cat			692
Arg Pro Ala Asn Gln Phe Val Pro Arg Leu Tyr Gly Phe Lys Ile His			
180	185	190	
cca atg gcc tac cag ctg cag ctc caa gcc gcc agc aac ttc aag agc			740
Pro Met Ala Tyr Gln Leu Gln Leu Gln Ala Ala Ser Asn Phe Lys Ser			
195	200	205	
cca gtc aag acg att cgc tga gtgccctccc acctcctctg cctgtgacac cacc			795
Pro Val Lys Thr Ile Arg			
210			
gtccctccgc tgccaccctt tcaggaagtc tatggttttt agttttaaat aaaggaattg			855
ttactgtggt ggggatatga aataaaggaa gagaaggcta aaaaaaaaaa aaaaaaccga			915
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23/26

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&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; siRNA for inhibiting human kasein kinase 2 beta subunit RNA

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21

&lt;210&gt; 21

24/26

&lt;211&gt; 21

&lt;212&gt; RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; siRNA for inhibiting human kasein kinase 2 beta subunit RNA

&lt;400&gt; 21

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21

&lt;210&gt; 22

&lt;211&gt; 21

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&lt;220&gt;

&lt;223&gt; siRNA for inhibiting human kasein kinase 2 beta subunit RNA

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&lt;213&gt; Artificial Sequence

&lt;220&gt;

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&lt;400&gt; 23

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&lt;210&gt; 24

&lt;211&gt; 21



25/26

&lt;212&gt; RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; siRNA for inhibiting rat kasein kinase 2 beta subunit RNA

&lt;400&gt; 24

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&lt;210&gt; 25

&lt;211&gt; 21

&lt;212&gt; RNA

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&lt;210&gt; 26

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; substrate of kasein kinase 2 used for determination of kasein kinase 2 activity

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&lt;210&gt; 27

26/26

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<212> PRT

<213> Artificial Sequence

<220>

<223> substrate of kasein kinase 2 used for determination of kasein kinase 2 activity

<400> 27

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5